

SEQUENCE LISTING

<110> KITAMURA, TOSHIO
FUJIO, KEISHI

<120> CYTOKINE RECEPTOR-LIKE PROTEINS

<130> 084335/0143

<140> 09/913,728

<141> 2001-08-17

<150> JP 1999-041936

<151> 1999-02-19

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 1278

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (59)..(1135)

<400> 1

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Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala
   1               5               10               15

gca gcg gcg gcg gcg gcg gtg acg tca cgg ggt gat gtc aca gtc gtc      154
Ala Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
           20               25               30

tgc cat gac ctg gag acg gtg gag gtc acg tgg ggc tcg ggc ccc gac      202
Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
           35               40               45

cac cac ggc gcc aac ttg agc ctg gag ttc cgt tat ggt act ggc gcc      250
His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
           50               55               60

ctg caa ccc tgc ccg cga tat ttc ctg tcc ggc gct ggt gtc act tcc      298
Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
           65               70               75               80

ggg tgc atc ctc ccc gcg gcg agg gcg ggg ctg ctg gag ctg gca ctg      346
Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
           85               90               95

cgc gac gga ggc ggg gcc atg gtg ttt aag gct agg cag cgc gcg tcc      394
Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
           100              105              110

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gcc tgg ctg aag ccc cgc cca cct tgg aat gtg acg ctg ctc tgg aca	442
Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr	
115 120 125	
cca gac ggg gac gtg act gtc tcc tgg cct gcc cac tcc tac ctg ggc	490
Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly	
130 135 140	
ctg gac tac gag gtg cag cac cgg gag agc aat gac gat gag gac gcc	538
Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala	
145 150 155 160	
tgg cag acg acc tca ggg ccc tgc tgt gac ttg aca gtg ggc ggg ctc	586
Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu	
165 170 175	
gac ccc gcg cgc tgc tat gac ttc cgg gtt cgg gcg tcg ccc cgg gcc	634
Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala	
180 185 190	
gcg cac tat ggc ctg gag gcg cag cct agc gag tgg aca gcg gtg aca	682
Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr	
195 200 205	
agg ctt tcc ggg gca gca tcc gcg gcc tcc tgt acc gca agc ccc gcc	730
Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala	
210 215 220	
cca tcc ccg gcc ctg gcc ccg ccc ctc ctg ccc ctg ggc tgc ggc cta	778
Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu	
225 230 235 240	
gca gcg ctg ctg aca ctg tcc ctg ctc ctg gcc gcc ctg agg ctt cgc	826
Ala Ala Leu Leu Thr Leu Ser Leu Leu Leu Ala Ala Leu Arg Leu Arg	
245 250 255	
agg gtg aaa gat gcg ctg ctg ccc tgc gtc cct gac ccc agc ggc tcc	874
Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser	
260 265 270	
ttc cct gga ctc ttt gag aag cat cac ggg aac ttc cag gcc tgg att	922
Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile	
275 280 285	
gcg gac gcc cag gcc aca gcc ccg cca gcc agg acc gag gag gaa gat	970
Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp	
290 295 300	
gac ctc atc cac ccc aag gct aag agg gtg gag ccc gag gac ggc acc	1018
Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr	
305 310 315 320	
tcc ctc tgc acc gtg cca agg cca ccc agc ttc gag cca agg ggg ccg	1066
Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro	
325 330 335	

gga ggc ggg gcc atg gtg tca gtg ggc ggg gcc acg ttc atg gtg ggc 1114
 Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly
 340 345 350

gac agc ggc tac atg acc ctg tgaccttgaa gtcactgccca gtctatactt 1165
 Asp Ser Gly Tyr Met Thr Leu
 355

caggctgagg tcacttcctg tctttaaata attcaaactc acaaatcctg tgccctgtctg 1225
 tatgcaaatg tggtcacgaa tattcaaata aaatgcaaat gctatgctaa aaa 1278

<210> 2
 <211> 359
 <212> PRT
 <213> Mus musculus

<400> 2
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 1 5 10 15
 Ala Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
 20 25 30
 Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
 35 40 45
 His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
 50 55 60
 Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
 65 70 75 80
 Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
 85 90 95
 Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
 100 105 110
 Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr
 115 120 125
 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
 130 135 140
 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
 145 150 155 160
 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu
 165 170 175
 Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala
 180 185 190
 Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr
 195 200 205

Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala
 210 215 220
 Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu
 225 230 235 240
 Ala Ala Leu Leu Thr Leu Ser Leu Leu Leu Ala Ala Leu Arg Leu Arg
 245 250 255
 Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser
 260 265 270
 Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile
 275 280 285
 Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp
 290 295 300
 Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr
 305 310 315 320
 Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro
 325 330 335
 Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly
 340 345 350
 Asp Ser Gly Tyr Met Thr Leu
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<210> 3
 <211> 804
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (98)..(661)

<400> 3
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 Met Ala Trp Ala Leu Ala
 1 5
 gtc atc ctc ctg cct cgg ctc ctt acg gcg gca gcg gcg gcg gcg gcg 163
 Val Ile Leu Leu Pro Arg Leu Leu Thr Ala Ala Ala Ala Ala Ala
 10 15 20
 gtg acg tca cgg ggt gat gtc aca gtc gtc tgc cat gac ctg gag acg 211
 Val Thr Ser Arg Gly Asp Val Thr Val Val Cys His Asp Leu Glu Thr
 25 30 35
 gtg gag gtc acg tgg ggc tcg ggc ccc gac cac cac ggc gcc aac ttg 259
 Val Glu Val Thr Trp Gly Ser Gly Pro Asp His His Gly Ala Asn Leu
 40 45 50

agc ctg gag ttc cgt tat ggt act ggc gcc ctg caa ccc tgc ccg cga 307
 Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala Leu Gln Pro Cys Pro Arg
 55 60 65 70

tat ttc ctg tcc ggc gct ggt gtc act tcc ggg tgc atc ctc ccc gcg 355
 Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser Gly Cys Ile Leu Pro Ala
 75 80 85

gcg agg gcg ggg ctg ctg gag ctg gca ctg cgc gac gga ggc ggg gcc 403
 Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu Arg Asp Gly Gly Gly Ala
 90 95 100

atg gtg ttt aag gct agg cag cgc gcg tcc gcc tgg ctg aag ccc cgc 451
 Met Val Phe Lys Ala Arg Gln Arg Ala Ser Ala Trp Leu Lys Pro Arg
 105 110 115

cca cct tgg aat gtg acg ctg ctc tgg aca cca gac ggg gac gtg act 499
 Pro Pro Trp Asn Val Thr Leu Leu Trp Thr Pro Asp Gly Asp Val Thr
 120 125 130

gtc tcc tgg cct gcc cac tcc tac ctg ggc ctg gac tac gag gtg cag 547
 Val Ser Trp Pro Ala His Ser Tyr Leu Gly Leu Asp Tyr Glu Val Gln
 135 140 145 150

cac cgg gag agc aat gac gat gag gac gcc tgg cag acg acc tca ggg 595
 His Arg Glu Ser Asn Asp Asp Glu Asp Ala Trp Gln Thr Thr Ser Gly
 155 160 165

ccc tgc tgt gac ttg aca gtg ggc ggg gcc acg ttc atg gtg ggc gac 643
 Pro Cys Cys Asp Leu Thr Val Gly Gly Ala Thr Phe Met Val Gly Asp
 170 175 180

agc ggc tac atg acc ctg tgaccttgaa gtcactgccca gtctatactt 691
 Ser Gly Tyr Met Thr Leu
 185

caggctgagg tcacttcctg tctttaaata attcaaactc acaaatcctg tgccctgtctg 751

tatgcaaagt tggtcacgaa tattcaaata aaatgcaaatt gctatgctaa aaa 804

<210> 4

<211> 188

<212> PRT

<213> Mus musculus

<400> 4

Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala
 1 5 10 15

Ala Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
 20 25 30

Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
 35 40 45

His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
 50 55 60
 Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
 65 70 75 80
 Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
 85 90 95
 Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
 100 105 110
 Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr
 115 120 125
 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
 130 135 140
 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
 145 150 155 160
 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Ala
 165 170 175
 Thr Phe Met Val Gly Asp Ser Gly Tyr Met Thr Leu
 180 185

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
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19

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

ggtgatgtca cagtcgtctg ccatg

25

<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8

acggtccgca ggagtagcag taa

23

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

aaagaattcc cgcccctcct gccctgggc

30

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

gctggcggcc gcacctgcag gcgc

24

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

aaagaattcg ggggctgtat catggac

27

<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

aaagaattcg ggggtccaggt cgctagg

27

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

ggtagggaat tccggaattt cctcgagatg

30

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

aaagaattcc caggcgggtct cggtaggcgg

30

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

aaagaattcg ttaacccgcc cctcctgccc ctgggg

36

<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

aaagcggccg cctcgagcca ggctggaag ttccc

35

<210> 17

<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
aaactcgagc tgtaccagaa tgatggc 27

<210> 18
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
aaagcggccg ctcacttgtc agagcaagcc acatagct 38

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
aaagcggccg ctcagtcac agagcaagcc acatagct 38

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
aaagcggccg ctcagtcctt agagcaagcc acatagct 38

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
aaagcggccg ctcagtaac agagcaagcc acatagct 38

<210> 22
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 aaagaattcg ggggctgtat catggac 27

<210> 23
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 aaagttaacg ggtccaggt cgctagg 27

<210> 24
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 24
 Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 25
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 25
 agggaattcc ggaatttcct cgagatc 27

<210> 26
 <211> 59
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 26
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<210> 27
 <211> 255
 <212> PRT
 <213> Mus sp.

<400> 27
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 Leu Leu Leu Arg Ala Gly Trp Ser Ser Lys Val Leu Met Ser Ser Ala
 20 25 30
 Asn Glu Asp Ile Lys Ala Asp Leu Ile Leu Thr Ser Thr Ala Pro Glu
 35 40 45
 His Leu Ser Ala Pro Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
 50 55 60
 Phe Asn Ile Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
 65 70 75 80
 Gln Ala Thr Asn Leu Thr Leu His Tyr Arg Tyr Lys Val Ser Asp Asn
 85 90 95
 Asn Thr Phe Gln Glu Cys Ser His Tyr Leu Phe Ser Lys Glu Ile Thr
 100 105 110
 Ser Gly Cys Gln Ile Gln Lys Glu Asp Ile Gln Leu Tyr Gln Thr Phe
 115 120 125
 Val Val Gln Leu Gln Asp Pro Gln Lys Pro Gln Arg Arg Ala Val Gln
 130 135 140
 Lys Leu Asn Leu Gln Asn Leu Val Ile Pro Arg Ala Pro Glu Asn Leu
 145 150 155 160
 Thr Leu Ser Asn Leu Ser Glu Ser Gln Leu Glu Leu Arg Trp Lys Ser
 165 170 175
 Arg His Ile Lys Glu Arg Cys Leu Gln Tyr Leu Val Gln Tyr Arg Ser
 180 185 190
 Asn Arg Asp Arg Ser Trp Thr Glu Leu Ile Val Asn His Glu Pro Arg
 195 200 205
 Phe Ser Leu Pro Ser Val Asp Glu Leu Lys Arg Tyr Thr Phe Arg Val
 210 215 220
 Arg Ser Arg Tyr Asn Pro Ile Cys Gly Ser Ser Gln Gln Trp Ser Lys
 225 230 235 240
 Trp Ser Gln Pro Val His Trp Gly Ser His Thr Val Glu Glu Asn
 245 250 255

<210> 28
 <211> 63
 <212> PRT
 <213> Mus sp.

<220>
 <221> MOD_RES
 <222> (29)..(47)
 <223> Variable amino acid

<400> 28
 Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser Phe Pro Gly Leu Phe
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 Glu Lys His His Gly Asn Phe Gln Ala Trp Ile Ala Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
 35 40 45
 Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr Ser Leu Cys Thr
 50 55 60

<210> 29
 <211> 60
 <212> PRT
 <213> Mus sp.

<220>
 <221> MOD_RES
 <222> (29)..(44)
 <223> Variable amino acid

<400> 29
 Ile Trp Pro Gly Ile Pro Ser Pro Glu Ser Glu Phe Glu Gly Leu Phe
 1 5 10 15
 Thr Thr His Lys Gly Asn Phe Gln Leu Trp Leu Leu Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Pro Pro Ala
 35 40 45
 His Leu Glu Val Leu Ser Glu Pro Arg Trp Ala Val
 50 55 60

<210> 30
 <211> 58
 <212> PRT
 <213> Mus sp.

<220>
 <221> MOD_RES
 <222> (29)..(42)
 <223> Variable amino acid

<400> 30

Leu Lys Cys His Ile Pro Asp Pro Ser Glu Phe Phe Ser Gln Leu Ser
 1 5 10 15

Ser Gln His Gly Gly Asp Leu Gln Lys Trp Leu Ser Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Glu Ile Ser Pro Leu
 35 40 45

Glu Val Leu Asp Gly Asp Ser Lys Ala Val
 50 55

<210> 31

<211> 54

<212> PRT

<213> Mus sp.

<220>

<221> MOD_RES

<222> (19)..(38)

<223> Variable amino acid

<400> 31

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Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Thr Asp Val Ser Val Val Glu Ile Glu Ala
 35 40 45

Asn Asn Lys Lys Pro Cys
 50

<210> 32

<211> 74

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Type 1 Cytokine
 receptor

<220>

<221> MOD_RES

<222> (25)..(58)

<223> Variable amino acid

<400> 32

Trp Lys Glu Lys Ile Pro Asn Pro Ser Lys Ser Leu Leu Phe Gln Asp
 1 5 10 15

Gly Gly Lys Gly Leu Trp Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Asn Val Ser Pro Leu
 50 55 60

Thr Ile Glu Asp Pro Asn Ile Ile Arg Val
 65 70

<210> 33

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative
 peptide

<400> 33

Leu Glu Val Leu

1

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative
 peptide

<220>

<221> MOD_RES

<222> (3)

<223> Variable amino acid

<400> 34

Trp Ser Xaa Trp Ser

1

5